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RAW SEQUENCE LISTING

DATE: 02/04/2002

PATENT APPLICATION: US/09/918,951

TIME: 11:21:56

Input Set : N:\Crf3\RULE60\09918951.raw

Output Set: N:\CRF3\02042002\I918951.raw

1 <110> APPLICANT: Alland, David
 2 Bloom, Barry R.
 3 Jacobs Jr., William R.
 4 <120> TITLE OF INVENTION: iniB, iniA AND iniC GENES OF MYCOBACTERIA AND METHODS
 5 OF USE
 6 <130> FILE REFERENCE: 96700/491
 7 <140> CURRENT APPLICATION NUMBER: 09/918,951
 8 <141> CURRENT FILING DATE: 2001-07-31
 10 <150> PRIOR APPLICATION NUMBER: US/09/177,349
 11 <151> PRIOR FILING DATE: 1998-10-23
 13 <160> NUMBER OF SEQ ID NOS: 14
 14 <170> SOFTWARE: PatentIn Ver. 2.0

ENTERED

16 <210> SEQ ID NO: 1
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 18 <212> TYPE: DNA
 19 <213> ORGANISM: Mycobacterium tuberculosis
 20 <400> SEQUENCE: 1
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 24 <211> LENGTH: 5036
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Mycobacterium tuberculosis
 27 <400> SEQUENCE: 2
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 30 acgcccggcg acagcttctt cgattgaagg gaaatgaaga tgacctcgct tatcgattac 180
 31 atcctgagcc tgttccgcag cgaagacgcc gcccggtcgt tcgttgccgc tccgggacgg 240
 32 gccatgacca gtgccgggct gatcgatatc gcgccgcacc aaatctcatc ggtggcgggc 300
 33 aatgtggtgc cgggtctgaa tctgggtgcc ggcgaccca tgagcggatt gcggcaggcc 360
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 35 ggcgcggggg tggcaagcgt catcacgacc gatgtcggtg cgggcctggc tagcggactg 480
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 37 ggtcaggctc gcttggtgc ccaggtcggt ctgggtttta ctgccgtgat tgaggccgag 600
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50	ctgatccacg	gcggtaccgg	cggctatggc	ggcatgaacc	cgccagtga	cgatgcgcgg	1380
51	gcaccgcaag	ttccggcgcg	ggcccagccg	atgaccacgg	cggccgagca	cacgccggcg	1440
52	gttaccacaac	cgcagcacac	gccggtcgag	ccgccgggtcc	acgataagcc	gccgagccat	1500
53	tcggtgtttg	acgtcgggtca	cgagccgccc	gtgacgcaca	cgccgcccgc	gcccacgaa	1560
54	ctgccgtcgt	acggcctttt	cggactaccc	gggttctgat	tcgcgagccg	atttcacgaa	1620
55	ccggtgggga	cgttcattgt	ccccgccgtt	ttgtgcgcat	accgtgatct	gaggcgtaaa	1680
56	cgagcgagaa	agtggggcga	caagggtgacc	cagcccgatg	acccacgtcg	ggtcgggtgtg	1740
57	atcgtcgaac	tgatcgatca	cactatcgcc	atcgccaaac	tgaacgagcg	tggtgatcta	1800
58	gtacagcggg	tgacgcgggc	tcgccagcgg	atcaccgacc	cgcagggtccg	tgtggtgatc	1860
59	gccgggctgc	tcaaacaggg	caagagtcaa	ttgtctcaatt	cgttgctcaa	cctgcccgcg	1920
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61	ccgtcggccc	ggcttgtgct	ggccgcccgg	cccgcagcgg	caaccgcagc	ggttgacatt	2040
62	cccgtcgatg	acatcagcac	cgatgtgcgt	cgggctccgc	acgccggtgg	ccgcgaggtg	2100
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81	gccgggttga	tcctcggccg	gatggcatat	aaagaggaca	aacaaaaccg	gttgctgcgg	3240
82	gtgcgcagcg	aggccaaggc	caatgtgcgg	cgcttcgtcg	acgacatttc	gttcgtcgtc	3300
83	agcaaaacaat	cacgggatcg	gctcaagatg	atccagcgtc	tgctgcgcga	ccactaccgc	3360
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91	aggccaccgg	gattgtgacc	tggttcggcg	accgtccgac	accgcgggtc	accgccaacc	3840
92	atcgcgcgcg	tcgacgcgcc	aacgtgcgca	tcacccgctc	gggcgggctg	agtttcgacc	3900
93	tgcgagggat	caaccgcggc	gagctgatcg	acctggaaag	cgagtggcca	gccgaggaac	3960
94	tcacgcagcg	caccattgtt	gacaccccg	gaacgtcgtc	gttggcatgc	gatgcctccg	4020
95	agcgcacgtt	gcggctgctg	gtccccgcgg	acgggggtgc	tcgggtggat	gcgggtggtg	4080
96	tcctgttgcg	caccctgaac	gccgctgacg	tcgcgctgct	caaacagatc	ggtgggctgg	4140

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100     ccgcgcgcac actgcgccag accgagttca tcgcgctgcg caagctggcc ggtgccgagc 4380
101     gcaccgagct caatagggcc ctgctgagcg tggaccgttt tgtgcgccgg gacagtccgc 4440
102     taccggtgga cgcgggcatc cgtgcgcaat tgctcgagcg gttcggcatg ttcggcatcc 4500
103     ggatgtcgat tgccgtgctg gcggccggcg tgaccgattc gaccgggctg gccgccgaac 4560
104     tgctggagcg cagcgggctg gtggcgctgc gcaatgtgat agaccagcag ttcgcgcagc 4620
105     gctccgacat gcttaaggcg cataccgcct tggctctcct gcgccgattc gtgcagacgc 4680
106     atccggtgcc ggccgaccccg tacgtcattg ccgacatcga cccgttgcta gccgacaccc 4740
107     acgccttcga agaactccga atgctaagcc ttttgccttc gcgggcaacg acattgaacg 4800
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109     ggctgggcct ggatccccgcg aattctcgcg aggccccgcg cgccgcgctg gccgcagcgc 4920
110     aacactggcg tcgccgtgcg gcgcatccac tcaacgatcc gttcactacc agggcctgtc 4980
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113 <210> SEQ ID NO: 3

114 <211> LENGTH: 479

115 <212> TYPE: PRT

116 <213> ORGANISM: Mycobacterium tuberculosis

117 <400> SEQUENCE: 3

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121           20           25           30
122      Gly Leu Ile Asp Ile Ala Pro His Gln Ile Ser Ser Val Ala Ala Asn
123           35           40           45
124      Val Val Pro Gly Leu Asn Leu Gly Ala Gly Asp Pro Met Ser Gly Leu
125           50           55           60
126      Arg Gln Ala Val Ala Ala Arg His Gly Phe Ala Gln Asp Val Ala Asn
127           65           70           75           80
128      Val Gly Phe Ala Gly Asp Ala Gly Ala Gly Val Ala Ser Val Ile Thr
129           85           90           95
130      Thr Asp Val Gly Ala Gly Leu Ala Ser Gly Leu Gly Ala Gly Phe Leu
131           100          105          110
132      Gly Gln Gly Gly Leu Ala Leu Ala Ala Ser Ser Gly Gly Phe Gly Gly
133           115          120          125
134      Gln Val Gly Leu Ala Ala Gln Val Gly Leu Gly Phe Thr Ala Val Ile
135           130          135          140
136      Glu Ala Glu Val Gly Ala Gln Val Gly Ala Gly Leu Gly Ile Gly Thr
137           145          150          155          160
138      Gly Leu Gly Ala Gln Ala Gly Met Gly Phe Gly Gly Gly Val Gly Leu
139           165          170          175
140      Gly Leu Gly Gly Gln Ala Gly Gly Val Ile Gly Gly Ser Ala Ala Gly
141           180          185          190
142      Ala Ile Gly Ala Gly Val Gly Gly Arg Leu Gly Gly Asn Gly Gln Ile
143           195          200          205
144      Gly Val Ala Gly Gln Gly Ala Val Gly Ala Gly Val Gly Ala Gly Val
145           210          215          220
146      Gly Gly Gln Ala Gly Ile Ala Ser Gln Ile Gly Val Ser Ala Gly Gly

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147      225      230      235      240
148 Gly Leu Gly Gly Val Gly Asn Val Ser Gly Leu Thr Gly Val Ser Ser
149      245      250      255
150 Asn Ala Val Leu Ala Ser Asn Ala Ser Gly Gln Ala Gly Leu Ile Ala
151      260      265      270
152 Ser Glu Gly Ala Ala Leu Asn Gly Ala Ala Met Pro His Leu Ser Gly
153      275      280      285
154 Pro Leu Ala Gly Val Gly Val Gly Gly Gln Ala Gly Ala Ala Gly Gly
155      290      295      300
156 Ala Gly Leu Gly Phe Gly Ala Val Gly His Pro Thr Pro Gln Pro Ala
157      305      310      315      320
158 Ala Leu Gly Ala Ala Gly Val Val Ala Lys Thr Glu Ala Ala Ala Gly
159      325      330      335
160 Val Val Gly Gly Val Gly Gly Ala Thr Ala Ala Gly Val Gly Gly Ala
161      340      345      350
162 His Gly Asp Ile Leu Gly His Glu Gly Ala Ala Leu Gly Ser Val Asp
163      355      360      365
164 Thr Val Asn Ala Gly Val Thr Pro Val Glu His Gly Leu Val Leu Pro
165      370      375      380
166 Ser Gly Pro Leu Ile His Gly Gly Thr Gly Gly Tyr Gly Gly Met Asn
167      385      390      395      400
168 Pro Pro Val Thr Asp Ala Pro Ala Pro Gln Val Pro Ala Arg Ala Gln
169      405      410      415
170 Pro Met Thr Thr Ala Ala Glu His Thr Pro Ala Val Thr Gln Pro Gln
171      420      425      430
172 His Thr Pro Val Glu Pro Pro Val His Asp Lys Pro Pro Ser His Ser
173      435      440      445
174 Val Phe Asp Val Gly His Glu Pro Pro Val Thr His Thr Pro Pro Ala
175      450      455      460
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177      465      470      475
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 640
181 <212> TYPE: PRT
182 <213> ORGANISM: Mycobacterium tuberculosis
183 <400> SEQUENCE: 4
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186 Ala Arg Lys Trp Gly Asp Thr Val Thr Gln Pro Asp Asp Pro Arg Arg
187      20      25      30
188 Val Gly Val Ile Val Glu Leu Ile Asp His Thr Ile Ala Ile Ala Lys
189      35      40      45
190 Leu Asn Glu Arg Gly Asp Leu Val Gln Arg Leu Thr Arg Ala Arg Gln
191      50      55      60
192 Arg Ile Thr Asp Pro Gln Val Arg Val Val Ile Ala Gly Leu Leu Lys
193      65      70      75      80
194 Gln Gly Lys Ser Gln Leu Leu Asn Ser Leu Leu Asn Leu Pro Ala Ala
195      85      90      95
196 Arg Val Gly Asp Asp Glu Ala Thr Val Val Ile Thr Val Val Ser Tyr

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200	Thr	Thr	Ala	Ala	Val	Asp
201		130		135		140
202	Arg	Arg	Ala	Pro	His	Ala
203	145			150		155
204	Gly	Ala	Pro	Ser	Pro	Leu
205				165		170
206	Pro	Gly	Val	Gly	Gly	Leu
207				180		185
208	Leu	Leu	Pro	Glu	Ala	Asp
209				195		200
210	Glu	Phe	Thr	Glu	Pro	Glu
211				210		215
212	Cys	Pro	Val	Gly	Ala	Val
213	225					230
214	Trp	Arg	Glu	Ile	Val	Asn
215						245
216	Val	Pro	Met	Pro	Ile	Ile
217						260
218	Val	Thr	Leu	Asn	Asp	Lys
219						275
220	Ile	Val	Lys	Phe	Leu	Ser
221						290
222	Val	Arg	Ala	Gly	Val	Leu
223	305					310
224	Ala	Val	Ser	Leu	Gly	Ser
225						325
226	Arg	Asp	Arg	Leu	Ala	Ser
227						340
228	Gln	Ala	Val	Gln	Gln	Thr
229						355
230	Phe	Asn	Asp	Leu	Thr	Ala
231						370
232	Arg	Thr	Val	Thr	Glu	Asp
233	385					390
234	Thr	Ala	His	Trp	Ala	Glu
235						405
236	Thr	Ala	Val	Gly	Asp	Asn
237						420
238	Leu	Ala	Asp	Val	Ala	Arg
239						435
240	Val	Leu	Ser	Ala	Glu	Leu
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242	Arg	Leu	Lys	Ala	Leu	Gly
243	465					470
244	His	Lys	Met	Ile	Ile	Gly
245						485

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